

SEQUENCE LISTING

<110> GRIESBECK, OLIVER
HEIM, NICOLA

<120> NOVEL GENETICALLY ENCODED BIOINDICATORS OF CALCIUM-IONS

<130> 085449-0185

<140> 10/567,091

<141> 2008-07-21

<150> PCT/EP2004/008739

<151> 2004-08-04

<150> EP 03016691.2

<151> 2003-08-04

<160> 54

<170> PatentIn version 3.3

<210> 1

<211> 1863

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polynucleotide

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polypeptide

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
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Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
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Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
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Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
 245 250 255

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
 260 265 270

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
 275 280 285

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
 290 295 300

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
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Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
 325 330 335

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
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Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
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Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
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Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
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Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 405 410 415

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
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Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
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Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
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Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
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Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
500 505 510

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
515 520 525

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
530 535 540

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
545 550 555 560

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
565 570 575

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
580 585 590

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
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Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<211> 1902

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polynucleotide

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<210> 4

<211> 633

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

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 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Met Asp Asp Ile Tyr Lys Ala Ala Val
225 230 235 240

Glu Gln Leu Thr Glu Glu Gln Lys Asn Glu Phe Lys Ala Ala Phe Asp
245 250 255

Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile Ser Thr Lys Glu Leu
260 265 270

Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro Thr Pro Glu Glu Leu
275 280 285

Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly Ser Gly Thr Val Asp
290 295 300

Phe Asp Glu Phe Leu Val Met Met Val Arg Cys Met Lys Asp Asp Ser
305 310 315 320

Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu Phe Arg Met Phe Asp
325 330 335

Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu Leu Lys Ile Met Leu
340 345 350

Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp Ile Glu Glu Leu Met
355 360 365

Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile Asp Tyr Asp Glu Phe
370 375 380

Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met Val Ser Lys Gly Glu
385 390 395 400

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
405 410 415

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
420 425 430

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
435 440 445

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met
450 455 460

Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys
465 470 475 480

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
485 490 495

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
500 505 510

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
515 520 525

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
530 535 540

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe
545 550 555 560

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
565 570 575

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
580 585 590

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
595 600 605

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
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Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<210> 5
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
polynucleotide

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taa 1863

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<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic polypeptide

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
 225 230 235 240

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
 245 250 255

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
 260 265 270

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
 275 280 285

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
 290 295 300

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
 305 310 315 320

Ile Phe Ala Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
 325 330 335

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
 340 345 350

Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
 355 360 365

Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
 370 375 380

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
 385 390 395 400

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
 405 410 415

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
 420 425 430

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
 435 440 445

Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
 450 455 460

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 465 470 475 480

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
 485 490 495

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 500 505 510

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 515 520 525

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 530 535 540

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 545 550 555 560

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 565 570 575

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
 580 585 590

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
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Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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 <212> DNA
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 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

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aacttcaaga tccgccacaa catcgaggac ggcagcgtgc agctcgccga ccactaccag 1740
cagaacaccc ccatcggcga cggccccgtg ctgctgcccg acaaccacta cctgagctac 1800
cagtccgccc tgagcaaaga cccaacgag aagcgcgatc acatggtcct gctggagttc 1860
gtgaccgccc ccgggatcac tctcgcatg gacgagctgt acaagtaa 1908

```

<210> 8

<211> 635

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 8

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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1           5           10           15

```

```

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20           25           30

```

```

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35           40           45

```

```

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50           55           60

```

```

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65           70           75           80

```

```

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85           90           95

```

```

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100          105          110

```

```

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115          120          125

```

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala
 225 230 235 240

Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala
 245 250 255

Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys
 260 265 270

Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu
 275 280 285

Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr
 290 295 300

Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu
 305 310 315 320

Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile
 325 330 335

Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu
 340 345 350

Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp
 355 360 365

Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp
 370 375 380

Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser Lys
 385 390 395 400

Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp
 405 410 415

Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly
 420 425 430

Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly
 435 440 445

Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly
 450 455 460

Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp Phe
 465 470 475 480

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe
 485 490 495

Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu
 500 505 510

Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys
 515 520 525

Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser
 530 535 540

His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala
 545 550 555 560

Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala
 565 570 575

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
 580 585 590

Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro
 595 600 605

Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
 610 615 620

Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 625 630 635

<210> 9

<211> 1542

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 9

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ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc	300
ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg	360
gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac	420
aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac	480
ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc	540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac	600
tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcg tccatgggtc	660
ctgctggagt tcgtgaccgc cgcccgcatg ctaggccaga accccaccaa agaggagctg	720
gatgccatca tcgaggaggt ggacgaggat ggcagcgcca ccatcgactt cgaggagttc	780
ctggtgatga tgggtgcgcca gatgaaagag gacgccgagc tcatggtgag caagggcgag	840
gagctgttca ccggggtggt gcccatcctg gtcgagctgg acggcgacgt aaacggccac	900
aagttcagcg tgtccggcga gggcgagggc gatgccacct acggcaagct gaccctgaag	960
ttcatctgca ccaccggcaa gctgcccgtg ccctggccca ccctcgtgac caccttcggc	1020

```

tacggcctga tgtgcttcgc ccgctacccc gaccacatgc gccagcacga cttcttcaag 1080
tccgccatgc ccgaaggcta cgtccaggag cgcaccatct tcttcaagga cgacggcaac 1140
tacaagaccc gcgccgaggt gaagttcgag ggcgacaccc tggatgaaccg catcgagctg 1200
aagggcatcg acttcaagga ggacggcaac atcctggggc acaagctgga gtacaactac 1260
aacagccaca acgtctatat catggccgac aagcagaaga acggcatcaa ggccaacttc 1320
aagatccgcc acaacatcga ggacggcagc gtgcagctcg ccgaccacta ccagcagaac 1380
accccatcg gcgacggccc cgtgctgctg ccgacaacc actacctgag ctaccagtcc 1440
gccctgagca aagaccccaa cgagaagcgc gatcacatgg tcctgctgga gttcgtgacc 1500
gccgccggga tcaactctcg catggacgag ctgtacaagt aa 1542

```

<210> 10

<211> 513

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 10

```

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1           5           10           15

```

```

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
          20           25           30

```

```

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35           40           45

```

```

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50           55           60

```

```

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65           70           75           80

```

```

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85           90           95

```

```

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100          105          110

```

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu
 225 230 235 240

Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp
 245 250 255

Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala
 260 265 270

Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 275 280 285

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 290 295 300

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 305 310 315 320

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 325 330 335

Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His
 340 345 350

Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 355 360 365

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 370 375 380

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 385 390 395 400

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 405 410 415

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 420 425 430

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 435 440 445

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 450 455 460

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 465 470 475 480

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 485 490 495

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 500 505 510

Lys

<210> 11
 <211> 2469
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 11
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ggcaagctga	ccctgaagtt	catctgcacc	accggcaagc	tgcccgtgcc	ctggcccacc	180
ctcgtgacca	ccctgacctg	gggcgtgcag	tgtttcagcc	gctaccccga	ccacatgaag	240
cagcacgact	tcttcaagtc	cgccatgccc	gaaggctacg	tccaggagcg	taccatcttc	300
ttcaaggacg	acggcaacta	caagaccgcg	gccgaggtga	agttcgaggg	cgacaccctg	360
gtgaaccgca	tcgagctgaa	gggcatcgac	ttcaaggagg	acggcaacat	cctggggcac	420
aagctggagt	acaactacat	cagccacaac	gtctatatca	ccgccgacaa	gcagaagaac	480
ggcatcaagg	cccacttcaa	gatccgccac	aacatcgagg	acggcagcgt	gcagctcgcc	540
gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgctgctgcc	cgacaaccac	600
tacctgagca	cccagtcgcg	cctgagcaaa	gaccccaacg	agaagcgcg	tcacatggtc	660
ctgctggagt	tcgtgaccgc	cgcccgcgatg	ctaattggcgt	caatgacgga	ccagcaggcg	720
gaggccccgc	ccttcctcag	cgaggagatg	attgctgagt	tcaaagctgc	ctttgacatg	780
tttgatgcgg	acggtggtgg	ggacatcagc	accaaggagt	tgggcacggt	gatgaggatg	840
ctggggccaga	acccccacaa	agaggagctg	gatgccatca	tcgaggaggt	ggacgaggat	900
ggcagcggca	ccatcgactt	cgaggagttc	ctggtgatga	tggtgcgcca	gatgaaagag	960
gacgccaaag	gcaagtctga	ggaggagctg	gccaaactgct	tccgcatctt	cgacaagaac	1020
gctgatgggt	tcatcgacat	cgaggagctg	ggtgagattc	tcagggccac	tggggagcac	1080
gtcatcgagg	aggacataga	agacctcatg	aaggattcag	acaagaacaa	tgacggccgc	1140
attgacttcg	atgagttcct	gaagatgatg	gaggggtgtg	aggagctcgg	cggcattgtt	1200
gatgaagaga	aaaagcgtcg	tgagccacc	gcccgtcgtc	agcacctgaa	gagtgtctatg	1260
ctccagcttg	ctgtcactga	aatagaaaaa	gaagcagctg	ctaaagaagt	ggaaaagcaa	1320
aactacctgg	cagagcatag	ccctcctctg	tccctcccag	ggtccatgca	ggaacttcag	1380
gaactgagca	aaaaacttca	tgccaagata	gactcagtgg	atgaggaaaag	gtatgacaca	1440
gaggtgaagc	tacagaagac	taacaaggag	ctggaggacc	tgagccagaa	gctgtttgac	1500
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ctgcgtgccc	tgctgggctc	caagcacaag	gtcaacatgg	acctccgggc	caacctgaag	1620
caagtcaaga	aggaggacac	ggagaaggag	aaggacctcc	gcgatgtggg	tgactggagg	1680
aagaacattg	aggagaaatc	tggcatggag	ggcaggaaga	agatgtttga	ggccggcgag	1740
tccgagctca	tggtgagcaa	gggcgaggag	ctgttcaccg	gggtgggtgcc	catcctggtc	1800

gagctggacg gcgacgtaaa cggccacaag ttcagcgtgt ccggcgaggg cgagggcgat 1860
 gccacctacg gcaagctgac cctgaagttc atctgcacca ccggcaagct gcccgtgccc 1920
 tggcccaccc tcgtgaccac cttcggctac ggctgatgt gcttcgcccc ctaccccgac 1980
 cacatgcgcc agcacgactt cttcaagtcc gccatgcccc aaggctacgt ccaggagcgc 2040
 accatcttct tcaaggacga cggcaactac aagaccgcg ccgaggtgaa gttcgagggc 2100
 gacaccctgg tgaaccgcat cgagctgaag ggcatcgact tcaaggagga cggcaacatc 2160
 ctggggcaca agctggagta caactacaac agccacaacg tctatatcat ggccgacaag 2220
 cagaagaacg gcatcaaggc caacttcaag atccgccaca acatcgagga cggcagcgtg 2280
 cagctcgccg accactacca gcagaacacc cccatcgggc acggccccgt gctgctgccc 2340
 gacaaccact acctgagcta ccagtcgcc ctgagcaaag accccaacga gaagcgcgat 2400
 cacatgggtc tctgaggatt cgtgaccgcc gccgggatca ctctcgcat ggacgagctg 2460
 tacaagtaa 2469

<210> 12
 <211> 822
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 12
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala
 225 230 235 240

Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala
 245 250 255

Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys
 260 265 270

Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu
 275 280 285

Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr
 290 295 300

Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu
 305 310 315 320

Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile
325 330 335

Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu
340 345 350

Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp
355 360 365

Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp
370 375 380

Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Gly Gly Met Ser
385 390 395 400

Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln His Leu
405 410 415

Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys Glu Ala
420 425 430

Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His Ser Pro
435 440 445

Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu Ser Lys
450 455 460

Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr Asp Thr
465 470 475 480

Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu Ser Gln
485 490 495

Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg
500 505 510

Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys
515 520 525

His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val Lys Lys
530 535 540

Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp Trp Arg
545 550 555 560

Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys Met Phe
565 570 575

Glu Ala Gly Glu Ser Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe
580 585 590

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly
595 600 605

His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly
610 615 620

Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro
625 630 635 640

Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala
645 650 655

Arg Tyr Pro Asp His Met Arg Gln His Asp Phe Phe Lys Ser Ala Met
660 665 670

Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly
675 680 685

Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val
690 695 700

Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile
705 710 715 720

Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile
725 730 735

Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg
740 745 750

His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln
755 760 765

Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr
770 775 780

Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp
 785 790 795 800

His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly
 805 810 815

Met Asp Glu Leu Tyr Lys
 820

<210> 13
 <211> 1959
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 13
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 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
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 ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgaggg cgacaccctg 360
 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480
 ggcataagg ccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
 gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600
 tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc 660
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 gccttcctca gcgaggagat gattgctgag ttcaaagctg cctttgacat gtttgatgcg 840
 gacggtggtg gggacatcag caccaaggag ttgggcacgg tgatgaggat gctgggccag 900
 aacccaccca aagaggagct ggatgccatc atcgaggagg tggacgagga tggcagcggc 960
 accatcgact tcgaggagtt cctggtgatg atggtgcgcc agatgaaaga ggacgccaaag 1020
 ggcaagtctg aggaggagct ggccaactgc ttccgcatct tcgacaagaa cgctgatggg 1080

```

ttcatcgaca tcgaggagct gggtagatt ctcagggcca ctggggagca cgtcatcgag 1140
gaggacatag aagacctcat gaaggattca gacaagaaca atgacggccg cattgacttc 1200
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ctgttcaccg gggtagtgcc catcctggtc gagctggacg gcgacgtaaa cggccacaag 1320
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ggcctgatgt gcttcgcccg ctaccccgac cacatgcgcc agcacgactt cttcaagtcc 1500
gccatgcccg aaggctacgt ccaggagcgc accatcttct tcaaggacga cggcaactac 1560
aagaccgcg ccgaggtgaa gttcgagggc gacaccctgg tgaaccgcat cgagctgaag 1620
ggcatcgact tcaaggagga cggcaacatc ctggggcaca agctggagta caactacaac 1680
agccacaacg tctatatcat ggccgacaag cagaagaacg gcatcaaggc caacttcaag 1740
atccgccaca acatcgagga cggcagcgtg cagctcgccg accactacca gcagaacacc 1800
cccatcgggc acggccccgt gctgctgccc gacaaccact acctgagcta ccagtccgcc 1860
ctgagcaaag accccaacga gaagcgcgat cacatggtcc tgctggagtt cgtgaccgcc 1920
gccgggatca ctctcggcac ggacgagctg tacaagtaa 1959

```

```

<210> 14
<211> 652
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

```

```

<400> 14
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1           5           10          15

```

```

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
      20           25           30

```

```

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
      35           40           45

```

```

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50           55           60

```

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Ala Asp Ala Met Leu Arg Ala Leu Leu
225 230 235 240

Gly Ser Lys His Lys Val Asn Gly Gly Ala Ser Met Thr Asp Gln Gln
245 250 255

Ala Glu Ala Arg Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys
260 265 270

Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr
275 280 285

Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys
290 295 300

Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly
305 310 315 320

Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys
325 330 335

Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg
340 345 350

Ile Phe Asp Lys Asn Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly
355 360 365

Glu Ile Leu Arg Ala Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu
370 375 380

Asp Leu Met Lys Asp Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe
385 390 395 400

Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln Glu Leu Met Val Ser
405 410 415

Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu
420 425 430

Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu
435 440 445

Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr
450 455 460

Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr
465 470 475 480

Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His Asp
485 490 495

Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
500 505 510

Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe
515 520 525

Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe
 530 535 540

Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn
 545 550 555 560

Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys
 565 570 575

Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu
 580 585 590

Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu
 595 600 605

Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp
 610 615 620

Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala
 625 630 635 640

Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 645 650

<210> 15
 <211> 1827
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 15
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 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
 ctctgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300
 ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgagg cgacaccctg 360
 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480

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ggcatcaagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
gaccactacc agcagaacac ccccatcggc gacggccccg tgctgctgcc cgacaaccac 600
tacctgagca cccagtccgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc 660
ctgctggagt tcgtgaccgc cgcccgcatg ctagacctga gccagaagct gtttgacctg 720
aggggcaagt tcaagaggcc acctctgcgc cgggtgcgca tgtctgctga tgccatgctg 780
cgtgccctgc tgggctccaa gcacaaggtc ggcagcggca gcatgctaata ggcgtcaatg 840
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gctgcctttg acatgtttga tgcggacggt ggtggggaca tcagcaccaa ggagttgggc 960
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gaggtggacg aggatggcag cggcaccatc gacttcgagg agttcctggt gatgatggtg 1080
cgccagatga aagaggacgc cgagctcatg gtgagcaagg gcgaggagct gttcaccggg 1140
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ggcgagggcg agggcgatgc cacctacggc aagctgacct tgaagttcat ctgcaccacc 1260
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ttcgcccgct accccgacca catgcgccag cagcacttct tcaagtccgc catgcccga 1380
ggctacgtcc aggagcgcac catcttcttc aaggacgacg gcaactacaa gaccgcgcgc 1440
gaggtgaagt tcgagggcga caccctggtg aaccgcatcg agctgaaggg catcgacttc 1500
aaggaggacg gcaacatcct ggggcacaag ctggagtaca actacaacag ccacaacgtc 1560
tatatcatgg ccgacaagca gaagaacggc atcaaggcca acttcaagat ccgccacaac 1620
atcgaggacg gcagcgtgca gtcgccgac cactaccagc agaacacccc catcggcgac 1680
ggccccgtgc tgctgccga caaccactac ctgagctacc agtccgccct gagcaaagac 1740
cccaacgaga agcgcgatca catggtcctg ctggagtctg tgaccgccgc cgggatcact 1800
ctcgcatgg acgagctgta caagtaa 1827

```

<210> 16

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 16

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Asp Leu Ser Gln Lys Leu Phe Asp Leu
225 230 235 240

Arg Gly Lys Phe Lys Arg Pro Pro Leu Arg Arg Val Arg Met Ser Ala
245 250 255

Asp Ala Met Leu Arg Ala Leu Leu Gly Ser Lys His Lys Val Gly Ser
260 265 270

Gly Ser Met Leu Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg
275 280 285

Ala Phe Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp
290 295 300

Met Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly
305 310 315 320

Thr Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp
325 330 335

Ala Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe
340 345 350

Glu Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Glu
355 360 365

Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
370 375 380

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
385 390 395 400

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
405 410 415

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
420 425 430

Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met
435 440 445

Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
450 455 460

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
465 470 475 480

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
485 490 495

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
500 505 510

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
515 520 525

Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
530 535 540

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
545 550 555 560

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
565 570 575

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
580 585 590

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
595 600 605

<210> 17

<211> 1869

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polynucleotide

<400> 17

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ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc	180
ctcgtgacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag	240
cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc	300

ttcaaggacg	acggcaacta	caagaccgcg	gccgaggtga	agttcgaggg	cgacaccctg	360
gtgaaccgca	tcgagctgaa	gggcatcgac	ttcaaggagg	acggcaacat	cctggggcac	420
aagctggagt	acaactacat	cagccacaac	gttatatatca	ccgccgacaa	gcagaagaac	480
ggcatcaagg	cccacttcaa	gatccgccac	aacatcgagg	acggcagcgt	gcagctcgcc	540
gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgctgctgcc	cgacaaccac	600
tacctgagca	cccagtccgc	cctgagcaaa	gaccccaacg	agaagcgcg	tcacatggtc	660
ctgctggagt	tcgtgaccgc	cgcccgcgtg	ctgctgacag	aagagcagaa	aaatgagttc	720
aaggcagcct	tcgacatctt	cgtgctgggc	gctgaggatg	gctgcatcag	caccaaggag	780
ctgggcaagg	tgatgaggat	gctgggccag	aacccccacc	ctgaggagct	gcaggagatg	840
atcgatgagg	tggacgagga	cggcagcggc	acggtggact	ttgatgagtt	cctgggtcatg	900
atggttcggt	gcatgaagga	cgacagcaaa	gggaaatctg	aggaggagct	gtctgacctc	960
ttccgcatgt	ttgacaaaaa	tgctgatggc	tacatcgacc	tggatgagct	gaagataatg	1020
ctgcaggcta	caggcgagac	catcacggag	gacgacatcg	aggaactcat	gaaggacgga	1080
gacaagaaca	acgacggccg	catcgactat	gatgagttcc	tggagtcat	gaaggggtgtg	1140
gaggagctca	tggtgagcaa	gggcgaggag	ctgttcaccg	gggtggtgcc	catcctggtc	1200
gagctggacg	gcgacgtaaa	cggccacaag	ttcagcgtgt	ccggcgaggg	cgagggcgat	1260
gccacctacg	gcaagctgac	cctgaagtcc	atctgcacca	ccggcaagct	gcccggtccc	1320
tggccccacc	tcgtgaccac	cttcggctac	ggcctgatgt	gcttcgcccc	ctacccccgac	1380
cacatgcgcc	agcacgactt	cttcaagtcc	gccatgcccc	aaggctacgt	ccaggagcgc	1440
accatcttct	tcaaggacga	cggcaactac	aagaccgcg	ccgaggtgaa	gttcgagggc	1500
gacaccctgg	tgaaccgcat	cgagctgaag	ggcatcgact	tcaaggagga	cggcaacatc	1560
ctggggcaca	agctggagta	caactacaac	agccacaacg	tctatatcat	ggccgacaag	1620
cagaagaacg	gcatcaaggc	caacttcaag	atccgccaca	acatcgagga	cggcagcgtg	1680
cagctcgccg	accactacca	gcagaacacc	cccatcggcg	acggccccgt	gctgctgccc	1740
gacaaccact	acctgagcta	ccagtccgcc	ctgagcaaa	accccaacga	gaagcgcgat	1800
cacatgggtc	tgctggagtt	cgtgaccgcc	gccgggatca	ctctcggcgt	ggacgagctg	1860
tacaagtaa						1869

<210> 18
 <211> 622
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 18
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 Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Leu Thr Glu Glu Gln Lys Asn Glu Phe
 225 230 235 240

Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu Asp Gly Cys Ile
 245 250 255

Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu Gly Gln Asn Pro
 260 265 270

Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val Asp Glu Asp Gly
 275 280 285

Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met Met Val Arg Cys
 290 295 300

Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu Leu Ser Asp Leu
 305 310 315 320

Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile Asp Leu Asp Glu
 325 330 335

Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile Thr Glu Asp Asp
 340 345 350

Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn Asp Gly Arg Ile
 355 360 365

Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val Glu Glu Leu Met
 370 375 380

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 385 390 395 400

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 405 410 415

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 420 425 430

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 435 440 445

Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln
 450 455 460

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 465 470 475 480

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 485 490 495

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 500 505 510

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 515 520 525

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 530 535 540

Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 545 550 555 560

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 565 570 575

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser
 580 585 590

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 595 600 605

Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 610 615 620

<210> 19

<211> 486

<212> DNA

<213> Homo sapiens

<400> 19

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ctgggcaagg tgatgaggat gctgggccag aacccacccc ctgaggagct gcaggagatg 180
atcgatgagg tggacgagga cggcagcggc acggtggact ttgatgagtt cctgggcatg 240
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ttccgcatgt ttgacaaaaa tgctgatggc tacatcgacc tggatgagct gaagataatg 360
ctgcaggcta caggcgagac catcacggag gacgacatcg aggagctcat gaaggacgga 420
gacaagaaca acgacggccg catcgactat gatgagttcc tggagttcat gaagggtgtg 480
gagtag 486

```

```

<210> 20
<211> 161
<212> PRT
<213> Homo sapiens

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<400> 20
Met Asp Asp Ile Tyr Lys Ala Ala Val Glu Gln Leu Thr Glu Glu Gln
1           5           10           15

```

```

Lys Asn Glu Phe Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu
20           25           30

```

```

Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu
35           40           45

```

```

Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val
50           55           60

```

```

Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met
65           70           75           80

```

```

Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Ser Glu Glu Glu
85           90           95

```

```

Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile
100          105          110

```

```

Asp Leu Asp Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile
115          120          125

```

```

Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn
130          135          140

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Asp Gly Arg Ile Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val
 145 150 155 160

Glu

<210> 21
 <211> 633
 <212> DNA
 <213> Homo sapiens

<400> 21
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 cgccgctcct ccaactaccg cgcttatgcc acggagccgc acgccaagaa aaaatctaag 120
 atctccgcct cgagaaaaatt gcagctgaag actctgctgc tgcagattgc aaagcaagag 180
 ctggagcgag aggcggagga gcggcgcgga gagaaggggc gcgctctgag caccgcgtgc 240
 cagccgctgg agttgaccgg gctgggcttc gcggagctgc aggacttggt ccgacagctc 300
 cacgcccgtg tggacaaggt ggatgaagag agatacgaca tagaggcaaa agtcaccaag 360
 aacatcacgg agattgcaga tctgactcag aagatctttg accttcgagg caagtttaag 420
 cggcccaccc tgcggagagt gaggatctct gcagatgcc tgatgcaggc gctgctgggg 480
 gcccgggcta aggagtccct ggacctgcgg gcccacctca agcaggtgaa gaaggaggac 540
 accgagaagg aaaaccggga ggtgggagac tggcggaaga acatcgatgc actgagtgga 600
 atggagggcc gcaagaaaaa gtttgagagc tga 633

<210> 22
 <211> 210
 <212> PRT
 <213> Homo sapiens

<400> 22
 Met Ala Asp Gly Ser Ser Asp Ala Ala Arg Glu Pro Arg Pro Ala Pro
 1 5 10 15

Ala Pro Ile Arg Arg Arg Ser Ser Asn Tyr Arg Ala Tyr Ala Thr Glu
 20 25 30

Pro His Ala Lys Lys Lys Ser Lys Ile Ser Ala Ser Arg Lys Leu Gln
 35 40 45

Leu Lys Thr Leu Leu Leu Gln Ile Ala Lys Gln Glu Leu Glu Arg Glu
 50 55 60

Ala Glu Glu Arg Arg Gly Glu Lys Gly Arg Ala Leu Ser Thr Arg Cys
65 70 75 80

Gln Pro Leu Glu Leu Thr Gly Leu Gly Phe Ala Glu Leu Gln Asp Leu
85 90 95

Cys Arg Gln Leu His Ala Arg Val Asp Lys Val Asp Glu Glu Arg Tyr
100 105 110

Asp Ile Glu Ala Lys Val Thr Lys Asn Ile Thr Glu Ile Ala Asp Leu
115 120 125

Thr Gln Lys Ile Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Thr Leu
130 135 140

Arg Arg Val Arg Ile Ser Ala Asp Ala Met Met Gln Ala Leu Leu Gly
145 150 155 160

Ala Arg Ala Lys Glu Ser Leu Asp Leu Arg Ala His Leu Lys Gln Val
165 170 175

Lys Lys Glu Asp Thr Glu Lys Glu Asn Arg Glu Val Gly Asp Trp Arg
180 185 190

Lys Asn Ile Asp Ala Leu Ser Gly Met Glu Gly Arg Lys Lys Lys Phe
195 200 205

Glu Ser
210

<210> 23
<211> 483
<212> DNA
<213> Homo sapiens

<400> 23
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ggcacggtga tgaggatgct gggccagaca cccaccaagg aggagctgga cgccatcatc 180
gaggaggtgg atgaggacgg cagcggcacc atcgacttcg aggagttctt ggtcatgatg 240
gtgcgccaga tgaaagagga cgcgaaaggg aagagcgagg aggagctggc cgagtgtctc 300

cgcatcttcg acaggaatgc agacggctac atcgacccgg aggagctggc tgagattttc 360
 agggcctccg gggagcacgt gactgacgag gagatcgaat ctctgatgaa agacggcgac 420
 aagaacaacg acggccgcat tgacttcgac gagttcctga agatgatgga gggcgtgcag 480
 taa 483

<210> 24
 <211> 160
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Thr Asp Gln Gln Ala Glu Ala Arg Ser Tyr Leu Ser Glu Glu Met
 1 5 10 15

Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala Asp Gly Gly
 20 25 30

Gly Asp Ile Ser Val Lys Glu Leu Gly Thr Val Met Arg Met Leu Gly
 35 40 45

Gln Thr Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu Glu Val Asp
 50 55 60

Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu Val Met Met
 65 70 75 80

Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu Glu Glu Leu
 85 90 95

Ala Glu Cys Phe Arg Ile Phe Asp Arg Asn Ala Asp Gly Tyr Ile Asp
 100 105 110

Pro Glu Glu Leu Ala Glu Ile Phe Arg Ala Ser Gly Glu His Val Thr
 115 120 125

Asp Glu Glu Ile Glu Ser Leu Met Lys Asp Gly Asp Lys Asn Asn Asp
 130 135 140

Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu Gly Val Gln
 145 150 155 160

<210> 25
 <211> 492
 <212> DNA
 <213> Gallus gallus

<400> 25
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 gctgagttca aagctgcctt tgacatgttt gatgcggacg gtggtgggga catcagcacc 120
 aaggagttgg gcacggtgat gaggatgctg ggccagaacc ccaccaaaga ggagctggat 180
 gccatcatcg aggaggtgga cgaggatggc agcggcacca tcgacttcga ggagttcctg 240
 gtgatgatgg tgcgccagat gaaagaggac gccaaaggga agtctgagga ggagctggcc 300
 aactgcttcc gcactcttga caagaacgct gatgggttca tcgacatcga ggagctgggt 360
 gagattctca gggccactgg ggagcacgtc atcgaggagg acatagaaga cctcatgaag 420
 gattcagaca agaacaatga cggccgcatt gacttcgatg agttcctgaa gatgatggag 480
 ggtgtgcagt aa 492

<210> 26
 <211> 163
 <212> PRT
 <213> Gallus gallus

<400> 26
 Met Ala Ser Met Thr Asp Gln Gln Ala Glu Ala Arg Ala Phe Leu Ser
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 Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met Phe Asp Ala
 20 25 30
 Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr Val Met Arg
 35 40 45
 Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala Ile Ile Glu
 50 55 60
 Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu Glu Phe Leu
 65 70 75 80
 Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly Lys Ser Glu
 85 90 95
 Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn Ala Asp Gly
 100 105 110

Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala Thr Gly Glu
 115 120 125

His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp Ser Asp Lys
 130 135 140

Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys Met Met Glu
 145 150 155 160

Gly Val Gln

<210> 27
 <211> 552
 <212> DNA
 <213> Gallus gallus

<400> 27
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 aagcaaaact acctggcaga gcattgccct cctctgtccc tcccaggatc catgcaggaa 180
 cttcaggaac tgtgcaaaaa gcttcatgcc aagatagact cagtggatga ggaaaggtat 240
 gacacagagg tgaagctaca gaagactaac aaggagctgg aggacctgag ccagaagctg 300
 tttgacctga ggggcaagtt caagaggcca cctctgcgcc gggtgcgcat gtctgctgat 360
 gccatgctgc gtgccctgct gggctccaag cacaagggtca acatggacct ccgggccaac 420
 ctgaagcaag tcaagaagga ggacacggag aaggagaagg acctccgcga tgtgggtgac 480
 tggaggaaga acattgagga gaaatctggc atggagggca ggaagaagat gtttgaggcc 540
 ggcgagtcct aa 552

<210> 28
 <211> 183
 <212> PRT
 <213> Gallus gallus

<400> 28
 Met Ser Asp Glu Glu Lys Lys Arg Arg Ala Ala Thr Ala Arg Arg Gln
 1 5 10 15

His Leu Lys Ser Ala Met Leu Gln Leu Ala Val Thr Glu Ile Glu Lys
 20 25 30

Glu Ala Ala Ala Lys Glu Val Glu Lys Gln Asn Tyr Leu Ala Glu His
 35 40 45

Cys Pro Pro Leu Ser Leu Pro Gly Ser Met Gln Glu Leu Gln Glu Leu
 50 55 60

Cys Lys Lys Leu His Ala Lys Ile Asp Ser Val Asp Glu Glu Arg Tyr
 65 70 75 80

Asp Thr Glu Val Lys Leu Gln Lys Thr Asn Lys Glu Leu Glu Asp Leu
 85 90 95

Ser Gln Lys Leu Phe Asp Leu Arg Gly Lys Phe Lys Arg Pro Pro Leu
 100 105 110

Arg Arg Val Arg Met Ser Ala Asp Ala Met Leu Arg Ala Leu Leu Gly
 115 120 125

Ser Lys His Lys Val Asn Met Asp Leu Arg Ala Asn Leu Lys Gln Val
 130 135 140

Lys Lys Glu Asp Thr Glu Lys Glu Lys Asp Leu Arg Asp Val Gly Asp
 145 150 155 160

Trp Arg Lys Asn Ile Glu Glu Lys Ser Gly Met Glu Gly Arg Lys Lys
 165 170 175

Met Phe Glu Ala Gly Glu Ser
 180

<210> 29
 <211> 486
 <212> DNA
 <213> Gallus gallus

<400> 29
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 aaggctgcct tcgacatctt cgtgctgggg gcagaggatg gctgcatcag caccaaggag 120
 ctggggaagg tgatgaggat gctggggcag aacccccaccc ctgaggagct gcaggagatg 180
 attgatgagg tggatgagga tggcagtggc actgtggact ttgatgagtt ccttggttatg 240
 atggttcggt gtatgaaaga tgacagcaaa ggaaaaactg aagaggagct ctcagatctc 300
 ttcaggatgt ttgataagaa tgctgatggc tacatcgatc ttgaggaact gaagatcatg 360

ctacaggcaa ctggagagac gatcactgag gatgacatag aagaactgat gaaagatggg 420
gacaaaaaca atgatggcag gattgactat gacgagttcc tggagttcat gaaggagatt 480
gaataa 486

<210> 30
<211> 161
<212> PRT
<213> Gallus gallus

<400> 30
Met Asp Asp Ile Tyr Lys Ala Ala Val Glu Gln Leu Thr Glu Glu Gln
1 5 10 15
Lys Asn Glu Phe Lys Ala Ala Phe Asp Ile Phe Val Leu Gly Ala Glu
20 25 30
Asp Gly Cys Ile Ser Thr Lys Glu Leu Gly Lys Val Met Arg Met Leu
35 40 45
Gly Gln Asn Pro Thr Pro Glu Glu Leu Gln Glu Met Ile Asp Glu Val
50 55 60
Asp Glu Asp Gly Ser Gly Thr Val Asp Phe Asp Glu Phe Leu Val Met
65 70 75 80
Met Val Arg Cys Met Lys Asp Asp Ser Lys Gly Lys Thr Glu Glu Glu
85 90 95
Leu Ser Asp Leu Phe Arg Met Phe Asp Lys Asn Ala Asp Gly Tyr Ile
100 105 110
Asp Leu Glu Glu Leu Lys Ile Met Leu Gln Ala Thr Gly Glu Thr Ile
115 120 125
Thr Glu Asp Asp Ile Glu Glu Leu Met Lys Asp Gly Asp Lys Asn Asn
130 135 140
Asp Gly Arg Ile Asp Tyr Asp Glu Phe Leu Glu Phe Met Lys Gly Val
145 150 155 160
Glu

<210> 31
 <211> 1878
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 31
 atggtgagca agggcgagga gctgttcacc ggggtggtgc ccatcctggt cgagctggac 60
 ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
 ctctgaccca ccctgacctg gggcgtgcag tgettcagcc gctaccccga ccacatgaag 240
 cagcagcact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300
 ttcaaggacg acggcaacta caagaccgcg gccgaggtga agttcgaggg cgacaccctg 360
 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480
 ggcattcaagg ccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
 gaccactacc agcagaacac ccccatcggc gacggccccg tgetgctgcc cgacaaccac 600
 tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcgga tcacatggtc 660
 ctgctggagt tcgtgaccgc cgcccgcatg ctgagcgatg aattgactaa ggagcaaact 720
 gcattactac gtaatgcatt taatgctttt gaccctgaaa aaaatggata tatcaacaca 780
 gctatggtgg gtacgatact tagcatgttg ggatcatcaac ttgatgatgc aactcttgct 840
 gacattatcg ctgaagtcga tgaggatggt tcgggccaac tcgaatttga agaatttacc 900
 accctggcag ccgcttcct tgtggaagag gacgctgaag ctatgatggc tgaattgaag 960
 gaagctttcc gcctttacga caaagaagga aatggatata taactactgg tgttcttcgt 1020
 gaaatcctgc gcgaactaga cgataaattg acaaatgacg acctggacat gatgattgag 1080
 gaaattgatt ccgatggatc gggactgtt gattttgatg aatttatgga agtaatgacc 1140
 ggtggcgacg acgagctcat ggtgagcaag ggcgaggagc tgttcaccgg ggtggtgccc 1200
 atcctggctg agctggacgg cgacgtaaac ggccacaagt tcagcgtgtc cggcgagggc 1260
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 cccgtgccct ggcccaccct cgtgaccacc ttccgctacg gcctgatgtg cttcgcccgc 1380
 taccctgacc acatgcgcca gcacgacttc ttcaagtcgg ccatgcccga aggctacgtc 1440

caggagcgca ccattttttt caaggacgac ggcaactaca agaccgcgc cgaggtgaag 1500
 ttcgagggcg acaccctggt gaaccgcatc gagctgaagg gcatcgactt caaggaggac 1560
 ggcaacatcc tggggcacia gctggagtac aactacaaca gccacaacgt ctatatcatg 1620
 gccgacaagc agaagaacgg catcaaggcc aacttcaaga tccgccacaa catcgaggac 1680
 ggagcggtgc agctcgccga ccactaccag cagaacaccc ccatcggcga cggccccgtg 1740
 ctgctgcccg acaaccacta cctgagctac cagtccgccc tgagcaaaga cccaacgag 1800
 aagcgcgatc acatggctct gctggagttc gtgaccgccc ccgggatcac tctcggcag 1860
 gacgagctgt acaagtaa 1878

<210> 32

<211> 625

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 32

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Arg Met Leu Ser Asp Glu Leu Thr Lys Glu Gln Thr
 225 230 235 240

Ala Leu Leu Arg Asn Ala Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly
 245 250 255

Tyr Ile Asn Thr Ala Met Val Gly Thr Ile Leu Ser Met Leu Gly His
 260 265 270

Gln Leu Asp Asp Ala Thr Leu Ala Asp Ile Ile Ala Glu Val Asp Glu
 275 280 285

Asp Gly Ser Gly Gln Ile Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala
 290 295 300

Arg Phe Leu Val Glu Glu Asp Ala Glu Ala Met Met Ala Glu Leu Lys
 305 310 315 320

Glu Ala Phe Arg Leu Tyr Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr
 325 330 335

Gly Val Leu Arg Glu Ile Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn
 340 345 350

Asp Asp Leu Asp Met Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly
 355 360 365

Thr Val Asp Phe Asp Glu Phe Met Glu Val Met Thr Gly Gly Asp Asp
 370 375 380

Glu Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
 385 390 395 400

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
 405 410 415

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
 420 425 430

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
 435 440 445

Thr Thr Phe Gly Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His
 450 455 460

Met Arg Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
 465 470 475 480

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
 485 490 495

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
 500 505 510

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
 515 520 525

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
 530 535 540

Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp
 545 550 555 560

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
 565 570 575

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
 580 585 590

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
 595 600 605

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
 610 615 620

Lys
 625

<210> 33
 <211> 1866
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 33
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 ggcgacgtaa acggccacag gttcagcgtg tccggcgagg gcgagggcga tgccacctac 120
 ggcaagctga ccctgaagtt catctgcacc accggcaagc tgcccgtgcc ctggcccacc 180
 ctctgtacca ccctgacctg gggcgtgcag tgcttcagcc gctaccccga ccacatgaag 240
 cagcacgact tcttcaagtc cgccatgccc gaaggctacg tccaggagcg taccatcttc 300
 ttcaaggacg acggcaacta caagaccgc gccgaggtga agttcgagg cgacaccctg 360
 gtgaaccgca tcgagctgaa gggcatcgac ttcaaggagg acggcaacat cctggggcac 420
 aagctggagt acaactacat cagccacaac gtctatatca ccgccgacaa gcagaagaac 480
 ggcataagg cccacttcaa gatccgccac aacatcgagg acggcagcgt gcagctcgcc 540
 gaccactacc agcagaacac cccatcggc gacggccccg tgctgctgcc cgacaaccac 600
 tacctgagca ccagtcctgc cctgagcaaa gaccccaacg agaagcgcg tccatgggtc 660
 ctgctggagt tcgtgaccgc cgcccgcatg ctgactaagg agcaaactgc attactacgt 720
 aatgcattta atgcttttga ccctgaaaaa aatggatata tcaacacagc tatggtgggt 780
 acgatactta gcatgttggg tcatcaactt gatgatgcaa ctcttgctga cattatcgct 840
 gaagtcgatg aggatggttc gggccaaatc gaatttgaag aatttaccac cctggcagcc 900
 cgcttccttg tggaagagga cgctgaagct atgatggctg aattgaagga agctttccgc 960
 ctttacgaca aagaaggaaa tggatatata actactggtg ttcttcgtga aatcctgcgc 1020

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gaactagacg ataaattgac aaatgacgac ctggacatga tgattgagga aattgattcc 1080
gatggatcgg gtactgttga ttttgatgaa tttatggaag taatgaccgg tggcgacgac 1140
gagctcatgg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctggtcgag 1200
ctggacggcg acgtaaacgg ccacaagttc agcgtgtccg gcgagggcga gggcgatgcc 1260
acctacggca agctgaccct gaagttcatc tgcaccaccg gcaagctgcc cgtgccctgg 1320
cccaccctcg tgaccacctt cggctacggc ctgatgtgct tcgcccgcta ccccgaccac 1380
atgcgccagc acgacttctt caagtccgcc atgcccgaag gctacgtcca ggagcgcacc 1440
atctttcttca aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac 1500
accctgggtga accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg 1560
gggcacaagc tggagtacaa ctacaacagc cacaacgtct atatcatggc cgacaagcag 1620
aagaacggca tcaaggccaa cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag 1680
ctcgccgacc actaccagca gaacaccccc atcggcgacg gccccgtgct gctgcccgac 1740
aaccactacc tgagctacca gtccgccctg agcaaagacc ccaacgagaa gcgcgatcac 1800
atggtcctgc tggagttcgt gaccgccgcc gggatcactc tcggcatgga cgagctgtac 1860
aagtaa 1866

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<210> 34
<211> 621
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic
      polypeptide

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<400> 34
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1           5           10          15

Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val Ser Gly
      20           25           30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
      35           40           45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
      50           55           60

```

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Arg Met Leu Thr Lys Glu Gln Thr Ala Leu Leu Arg
225 230 235 240

Asn Ala Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr
245 250 255

Ala Met Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp
260 265 270

Ala Thr Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly
275 280 285

Gln Ile Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val
290 295 300

Glu Glu Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg
305 310 315 320

Leu Tyr Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg
325 330 335

Glu Ile Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp
340 345 350

Met Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp Phe
355 360 365

Asp Glu Phe Met Glu Val Met Thr Gly Gly Asp Asp Glu Leu Met Val
370 375 380

Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu
385 390 395 400

Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly
405 410 415

Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr
420 425 430

Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly
435 440 445

Tyr Gly Leu Met Cys Phe Ala Arg Tyr Pro Asp His Met Arg Gln His
450 455 460

Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr
465 470 475 480

Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys
485 490 495

Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp
500 505 510

Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr
515 520 525

Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile
 530 535 540

Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln
 545 550 555 560

Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val
 565 570 575

Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys
 580 585 590

Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr
 595 600 605

Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 610 615 620

<210> 35
 <211> 465
 <212> DNA
 <213> Drosophila melanogaster

<400> 35
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 gaccctgaaa aaaatggata tatcaacaca gctatggtgg gtacgatact tagcatgttg 120
 ggtcatcaac ttgatgatgc aactcttgct gacattatcg ctgaagtcga tgaggatggt 180
 tcgggccaaa tcgaatttga agaatttacc accctggcag cccgcttcct tgtggaagag 240
 gacgctgaag ctatgatggc tgaattgaag gaagctttcc gcctttacga caaagaagga 300
 aatggatata taactactgg tgttcttcgt gaaatcctgc gcgaactaga cgataaattg 360
 acaaatgacg acctggacat gatgattgag gaaattgatt ccgatggatc ggggtactgtt 420
 gattttgatg aatttatgga agtaatgacc ggtggcgacg actaa 465

<210> 36
 <211> 154
 <212> PRT
 <213> Drosophila melanogaster

<400> 36
 Met Ser Asp Glu Leu Thr Lys Glu Gln Thr Ala Leu Leu Arg Asn Ala
 1 5 10 15

57

Phe Asn Ala Phe Asp Pro Glu Lys Asn Gly Tyr Ile Asn Thr Ala Met
20 25 30

Val Gly Thr Ile Leu Ser Met Leu Gly His Gln Leu Asp Asp Ala Thr
35 40 45

Leu Ala Asp Ile Ile Ala Glu Val Asp Glu Asp Gly Ser Gly Gln Ile
50 55 60

Glu Phe Glu Glu Phe Thr Thr Leu Ala Ala Arg Phe Leu Val Glu Glu
65 70 75 80

Asp Ala Glu Ala Met Met Ala Glu Leu Lys Glu Ala Phe Arg Leu Tyr
85 90 95

Asp Lys Glu Gly Asn Gly Tyr Ile Thr Thr Gly Val Leu Arg Glu Ile
100 105 110

Leu Arg Glu Leu Asp Asp Lys Leu Thr Asn Asp Asp Leu Asp Met Met
115 120 125

Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp Phe Asp Glu
130 135 140

Phe Met Glu Val Met Thr Gly Gly Asp Asp
145 150

<210> 37

<211> 468

<212> DNA

<213> Drosophila melanogaster

<400> 37

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aacagcttcg accaccagaa gaccggcagt atccccaccg aaatggtggc cgatatactc 120

cgtcttatgg gtcagccctt cgacaggcag atccttgacg agctgatgca cgaggctgat 180

gaggacaaat ccggtcgctt ggagttcgag gagttcgctc agctggctgc caagttcatc 240

gtagaggagg atgatgaggc catgcagaag gacgtgcgcg aggctttccg tctgtacgac 300

aagcagggca atggctacat tcccacctcc tgctgaagg agatcctcaa ggaactggac 360

gaccagctga ccgaacagga gctcgacatc atgattgagg aaatcgattc cgacggctct 420

ggcaccgttg attttgatga attcatggag atgatgactg gcgagtaa 468

<210> 38
 <211> 155
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 38
 Met Asp Asn Ile Asp Glu Asp Leu Thr Pro Glu Gln Ile Ala Val Leu
 1 5 10 15

Gln Lys Ala Phe Asn Ser Phe Asp His Gln Lys Thr Gly Ser Ile Pro
 20 25 30

Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp
 35 40 45

Arg Gln Ile Leu Asp Glu Leu Met His Glu Val Asp Glu Asp Lys Ser
 50 55 60

Gly Arg Leu Glu Phe Glu Glu Phe Val Gln Leu Ala Ala Lys Phe Ile
 65 70 75 80

Val Glu Glu Asp Asp Glu Ala Met Gln Lys Asp Val Arg Glu Ala Phe
 85 90 95

Arg Leu Tyr Asp Lys Gln Gly Asn Gly Tyr Ile Pro Thr Ser Cys Leu
 100 105 110

Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu
 115 120 125

Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp
 130 135 140

Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu
 145 150 155

<210> 39
 <211> 468
 <212> DNA
 <213> *Drosophila melanogaster*

<400> 39
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 aacagcttcg atcaccagaa gactggctcc atccccaccg agatggctgc cgacatcctg 120
 cgcctgatgg gtcagccctt cgacaagaag atcctggagg aactgatcga ggaggtcgat 180

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gaggacaagt ccggtcgctt ggaattcggc gagttcgtcc agctggctgc caagttcatc 240
gtggaggagg atgcggaggc catgcagaag gagctggccg aggcgttccg tttgtacgat 300
aagcagggca atggcttcat tcccaccacc tgctgaagg agatcctcaa ggagctggac 360
gaccagctga ccgaacagga gctggacatt atgatcgagg agatcgattc cgatggctcc 420
ggtacagtgg atttcgatga attcatggag atgatgactg gcgagtaa 468

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<210> 40

<211> 155

<212> PRT

<213> *Drosophila melanogaster*

<400> 40

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Met Ser Ser Val Asp Glu Asp Leu Thr Pro Glu Gln Ile Ala Val Leu
1           5           10           15

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```

Gln Lys Ala Phe Asn Ser Phe Asp His Gln Lys Thr Gly Ser Ile Pro
          20           25           30

```

```

Thr Glu Met Val Ala Asp Ile Leu Arg Leu Met Gly Gln Pro Phe Asp
          35           40           45

```

```

Lys Lys Ile Leu Glu Glu Leu Ile Glu Glu Val Asp Glu Asp Lys Ser
          50           55           60

```

```

Gly Arg Leu Glu Phe Gly Glu Phe Val Gln Leu Ala Ala Lys Phe Ile
          65           70           75           80

```

```

Val Glu Glu Asp Ala Glu Ala Met Gln Lys Glu Leu Ala Glu Ala Phe
          85           90           95

```

```

Arg Leu Tyr Asp Lys Gln Gly Asn Gly Phe Ile Pro Thr Thr Cys Leu
          100          105          110

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```

Lys Glu Ile Leu Lys Glu Leu Asp Asp Gln Leu Thr Glu Gln Glu Leu
          115          120          125

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```

Asp Ile Met Ile Glu Glu Ile Asp Ser Asp Gly Ser Gly Thr Val Asp
          130          135          140

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Phe Asp Glu Phe Met Glu Met Met Thr Gly Glu
          145          150          155

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<210> 41
 <211> 1833
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 polynucleotide

<400> 41
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<210> 42

<211> 610

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 42

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Met Gly Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn
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```

```

Gly Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln
20           25           30

```

```

Gly Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe
35           40           45

```

```

Ser Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe
50           55           60

```

```

Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn
65           70           75           80

```

```

Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly
85           90           95

```

```

Val Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile
100          105          110

```

```

Gly Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile
115          120          125

```

Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His
130 135 140

Pro Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser
145 150 155 160

Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His
165 170 175

Phe Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met
180 185 190

Phe Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly
195 200 205

Ile Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg
210 215 220

Met Leu Ser Glu Glu Met Ile Ala Glu Phe Lys Ala Ala Phe Asp Met
225 230 235 240

Phe Asp Ala Asp Gly Gly Gly Asp Ile Ser Thr Lys Glu Leu Gly Thr
245 250 255

Val Met Arg Met Leu Gly Gln Asn Pro Thr Lys Glu Glu Leu Asp Ala
260 265 270

Ile Ile Glu Glu Val Asp Glu Asp Gly Ser Gly Thr Ile Asp Phe Glu
275 280 285

Glu Phe Leu Val Met Met Val Arg Gln Met Lys Glu Asp Ala Lys Gly
290 295 300

Lys Ser Glu Glu Glu Leu Ala Asn Cys Phe Arg Ile Phe Asp Lys Asn
305 310 315 320

Ala Asp Gly Phe Ile Asp Ile Glu Glu Leu Gly Glu Ile Leu Arg Ala
325 330 335

Thr Gly Glu His Val Ile Glu Glu Asp Ile Glu Asp Leu Met Lys Asp
340 345 350

Ser Asp Lys Asn Asn Asp Gly Arg Ile Asp Phe Asp Glu Phe Leu Lys
355 360 365

Met Met Glu Gly Val Gln Glu Leu Met Ser Ser Gly Ala Leu Leu Phe
 370 375 380

His Gly Lys Ile Pro Tyr Val Val Glu Met Glu Gly Asn Val Asp Gly
 385 390 395 400

His Thr Phe Ser Ile Arg Gly Lys Gly Tyr Gly Asp Ala Ser Val Gly
 405 410 415

Lys Val Asp Ala Gln Phe Ile Cys Thr Thr Gly Asp Val Pro Val Pro
 420 425 430

Trp Ser Thr Leu Val Thr Thr Leu Thr Tyr Gly Ala Gln Cys Phe Ala
 435 440 445

Lys Tyr Gly Pro Glu Leu Lys Asp Phe Tyr Lys Ser Cys Met Pro Asp
 450 455 460

Gly Tyr Val Gln Glu Arg Thr Ile Thr Phe Glu Gly Asp Gly Asn Phe
 465 470 475 480

Lys Thr Arg Ala Glu Val Thr Phe Glu Asn Gly Ser Val Tyr Asn Arg
 485 490 495

Val Lys Leu Asn Gly Gln Gly Phe Lys Lys Asp Gly His Val Leu Gly
 500 505 510

Lys Asn Leu Glu Phe Asn Phe Thr Pro His Cys Leu Tyr Ile Trp Gly
 515 520 525

Asp Gln Ala Asn His Gly Leu Lys Ser Ala Phe Lys Ile Cys His Glu
 530 535 540

Ile Thr Gly Ser Lys Gly Asp Phe Ile Val Ala Asp His Thr Gln Met
 545 550 555 560

Asn Thr Pro Ile Gly Gly Gly Pro Val His Val Pro Glu Tyr His His
 565 570 575

Met Ser Tyr His Val Lys Leu Ser Lys Asp Val Thr Asp His Arg Asp
 580 585 590

Asn Met Ser Leu Lys Glu Thr Val Arg Ala Val Asp Cys Arg Lys Thr
 595 600 605

Tyr Leu
 610

<210> 43
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 43
 Gly Gly Ser Gly Gly
 1 5

<210> 44
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 44
 Met Leu Leu Ser Val Pro Leu Leu Leu Gly Leu Leu Gly Leu Ala Ala
 1 5 10 15

Ala Asp

<210> 45
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 45
 Lys Asp Glu Leu
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<210> 46
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 46

Met	Leu	Cys	Cys	Met	Arg	Arg	Thr	Lys	Gln	Val	Glu	Lys	Asn	Asp	Glu
1				5					10					15	

Asp	Gln	Lys	Ile
			20

<210> 47

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 47

Lys	Leu	Asn	Pro	Pro	Asp	Glu	Ser	Gly	Thr	Gly	Cys	Met	Ser	Cys	Lys
1				5					10					15	

Cys	Val	Leu	Ser
			20

<210> 48

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 48

Val	Tyr	Glu	Lys	Leu	Ser	Ser	Ile	Glu	Ser	Asp	Val
1				5					10		

<210> 49

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic peptide

<400> 49

Met	Gln	Ala	Ala	Thr	Leu	Pro	Leu	Asp	Asn	Ile	Ser	Tyr	Arg	Arg	Glu
1				5					10					15	

Ser Ala Ile

<210> 50
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 50
 gccgccacca tgg

13

<210> 51
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 51
 Lys Leu Asn Pro Pro Asp Glu Ser Gly Pro Gly Cys Met Ser Cys Lys
 1 5 10 15

Cys Val Leu Ser
 20

<210> 52
 <211> 20
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 52
 Met Gly Cys Cys Met Arg Arg Thr Lys Gln Val Glu Lys Asn Asp Glu
 1 5 10 15

Asp Gln Lys Ile
 20

<210> 53
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
peptide

<400> 53
Gly Gly Thr Gly Gly Ser
1 5

<210> 54
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 54
gccgccacca tggcc